Functional Genomics for Plant Secondary Metabolism

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Abstracts

For the last few decades scientists in the field of plant secondary metabolism have worked on; 1) discovery of new functional compounds, 2) identification of the metabolic pathways of secondary metabolites, 3) identification of genes for the enzymes catalyzing the pathways, 4) production of useful secondary metabolites in cell culture systems, 5) metabolic engineering of secondary metabolism at the whole plant level, and 6) scale-up of cell culture systems and purification of useful secondary metabolites for commercialization. This work has used labor-intensive, time-consuming conventional methods and empirical approaches.

Since a holistic approach to plant secondary metabolism on the basis of genomics, high throughput biology, and bioinformatics has been introduced, the paradigm of such research is under drastic change. New functional compounds can be discovered by HTS and the secondary metabolite pathways and genes involved in the pathways can be determined by functional genomic approaches in conjunction with data-mining tools. In addition, plants are capable of being metabolically engineered with 3-5, or even more, heterologous genes to produce useful secondary metabolites on a large scale. For example, a few heterologous genes under control of a promoter as an operon are to be introduced into a plastid where the gene products may be safely compartmentalized from degrading enzymes in the cytosol.

E-cell is actually a model-building kit. It is a set of software tools that allows a user to specify a cell's genes, proteins, and other molecules, describe their individual interactions, and then compute how they work together as a system. E-cell was pioneered by Masaru Tomita, a professor of bioinformatics at Keio University in Fujisawa. It should ultimately allow investigators to conduct experiments "in silico," offering a cheap, fast way to screen drug candidates, study the effects of mutations or toxins, or simply probe the networks that govern cell behavior (Normile, 1999). Tomita has just completed a model of human erythrocytes and is building other models of human mitochondria, signal transduction for chemotaxis in the bacterium *E. coli,* and gene expression networks in this bacterium's lactose operon (Butler, 1999). Although plant cells are genetically much more complicated than bacterial cells (rice genome: 430 megabase vs. *E. coli* genome: 4.6 megabase), it does seem possible to play with a plant e-cell "tamagotchi" in the near future. E-cell may depict a highly sophisticated metabolic engineering for production of useful crop compounds in the future.